## SEQUENCE PROTOCOL <110> Degussa AG 5 <120> Nucleotide sequences which code for the dep67 gene <130> 000565 BT 10 <140> <141> <160> 4 15 <170> PatentIn Ver. 2.1 <210> 1 <211> 1786 <212> DNA 20 <213> Corynebacterium glutamicum <220> <221> CDS <222> (259)..(1560) 25 <223> dep67 gene <400> 1 cggcgttttc cgagcgggtg tctagcgcaa cgagtgcgga accgcgttgt tgggcctggc 60 30 tggcgagcat gtgttttgcc acgtcgacgg cattgcgctc ggacttaaaa ttcaacgccg 120 cagatggtgc aagcagctgt gaaatgaggc gtagggcgcg gacgcgttcc agagaaagtg 180 caqqcataac ccctaaaata ccctqatctt ccccqtqtc ctqccccqt qtccacccct 240 35 gcqtacataa taggacgc atg gga aaa cat gag gtt gct cag cag acg gtt Met Gly Lys His Glu Val Ala Gln Gln Thr Val 1 40 ccg ggt cct tcg ccg gaa atg gaa gcg cag cgg cgt aaa gag ttg cgc Pro Gly Pro Ser Pro Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg aag cac aag gcc att gcc act ggc ctg ttg att ttt gct gcc gct gta 45 Lys His Lys Ala Ile Ala Thr Gly Leu Leu Ile Phe Ala Ala Val 30 tat ttt ctt tgc cgt ttc gtg gag acc cgt ccg ggt gaa act gca gcg Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala 50 45 tgg gta ggt ttt gtg cgc gct gcg gca gag gcc gga atg att ggc ggg 483 Trp Val Gly Phe Val Arg Ala Ala Glu Ala Gly Met Ile Gly Gly 55 ttg gcc gac tgg ttc gcg gtc acc gcg ctg ttc cgt cat cca ttg tgg Leu Ala Asp Trp Phe Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp

	ctg Leu	cct Pro	att Ile	ccg Pro 95	cac His	act Thr	gcg Ala	att Ile	atc Ile 100	ccg Pro	cgc Arg	aag Lys	aaa Lys	gac Asp 105	cag Gln	tta Leu	579
5	ggt Gly	gag Glu	gcc Ala 110	tta Leu	agc Ser	Gly ggg	ttt Phe	gtg Val 115	gly ggg	gat Asp	aac Asn	ttc Phe	cta Leu 120	aat Asn	gcc Ala	cag Gln	627
10					aaa Lys												675
15	gag Glu 140	tgg Trp	ctc Leu	gcc Ala	cag Gln	ccg Pro 145	gaa Glu	aac Asn	Gly 999	gag Glu	aaa Lys 150	gtt Val	tcg Ser	cgc Arg	gaa Glu	gtc Val 155	723
20	ggc Gly	aaa Lys	ttg Leu	acc Thr	gct Ala 160	aat Asn	att Ile	gtg Val	cgc Arg	gca Ala 165	atc Ile	gat Asp	ccg Pro	tca Ser	gat Asp 170	gct Ala	771
20	gaa Glu	gcg Ala	gtg Val	att Ile 175	aaa Lys	tct Ser	gcg Ala	gtg Val	atc Ile 180	gac Asp	aag Lys	ctt Leu	gcg Ala	gaa Glu 185	ccc Pro	acc Thr	819
25	tgg Trp	ggc Gly	cca Pro 190	cca Pro	gct Ala	ggg Gly	cgg Arg	ttg Leu 195	ctg Leu	gaa Glu	caa Gln	ctc Leu	ctc Leu 200	gcc Ala	gaa Glu	gca Ala	867
30					ttg Leu												915
35	cgt Arg 220	tgg Trp	gct Ala	ccc Pro	gag Glu	ccg Pro 225	ctg Leu	att Ile	gat Asp	cgc Arg	ctg Leu 230	ctc Leu	aac Asn	gag Glu	cgc Arg	cgc Arg 235	963
40	ccg Pro	att Ile	tgg Trp	gcg Ala	ccg Pro 240	aaa Lys	ttc Phe	act Thr	gcg Ala	cag Gln 245	ctg Leu	gtc Val	agc Ser	ggc Gly	aaa Lys 250	gtc Val	1011
10					ata Ile												1059
45	cac His	gag Glu	gcc Ala 270	cgc Arg	aaa Lys	tcg Ser	ctg Leu	cgc Arg 275	cga Arg	ttc Phe	ctt Leu	aat Asn	aaa Lys 280	ttg Leu	gcg Ala	caa Gln	1107
50	gac Asp	ctg Leu 285	cag Gln	cat His	gac Asp	cca Pro	ggc Gly 290	atg Met	att Ile	att Ile	aaa Lys	gtt Val 295	gaa Glu	gaa Glu	atc Ile	aaa Lys	1155
55	cgc Arg 300	gac Asp	atc Ile	atg Met	ggc	tcc Ser 305	ggc Gly	gcc Ala	atc Ile	gcg Ala	caa Gln 310	gcc Ala	gcg Ala	cca Pro	acc Thr	atc Ile 315	1203
	tgg Trp	gcg Ala	tca Ser	gcc Ala	tcc Ser 320	Glu	tcg Ser	ctc Leu	att Ile	gaa Glu 325	tcc Ser	gca Ala	gaa Glu	gat Asp	gag Glu 330	tca Ser	1251

5			_	_	_			_	gaa Glu 340	-	_		_				1299
_									cgg Arg								1347
10									gac Asp								1395
15					_			_	cga Arg		_	_	_	_	_		1443
20									aaa Lys								1491
25									gca Ala 420								1539
					ttc Phe		_	taad	ctago	gag t	aaco	catca	at gt	ccga	atgca	a	1590
30	aaag	gacga	itt c	ccato	cttgt	c ca	agto	ggago	c aat	gcag	gctt	ccga	agcto	cag o	ggtg	gccgtc	1650
	agto	gagt	ag d	gaag	gaago	et co	gtga	aagaa	a cto	etete	gaga	agga	aaco	ctt d	cagca	agctt	1710
35	aaaaccgaag ccagcgaagc cgtcgatcaa gcaaagtccg gctcctacct agatgccggt 17															1770	
	aaggaatteg eeegeg 178														1786		
40	<212	.> 43 !> PF	T	ebact	eriu	ım gl	utan	nicum	n								
45	<400 Met 1		Lys	His	Glu 5	Val	Ala	Gln	Gln	Thr 10	Val	Pro	Gly	Pro	Ser 15	Pro	
50	Glu	Met	Glu	Ala 20	Gln	Arg	Arg	Lys	Glu 25	Leu	Arg	Lys	His	Lys 30	Ala	Ile	
	Ala	Thr	Gly 35	Leu	Leu	Ile	Phe	Ala 40	Ala	Ala	Val	Tyr	Phe 45	Leu	Cys	Arg	
55	Phe	Val 50	Glu	Thr	Arg	Pro	Gly 55	Glu	Thr	Ala	Ala	Trp 60	Val	Gly	Phe	Val	
	Arg 65	Ala	Ala	Ala	Glu	Ala 70	Gly	Met	Ile	Gly	Gly 75	Leu	Ala	Asp	Trp	Phe	

	Ala	Val	Thr	Ala	Leu 85	Phe	Arg	His	Pro	Leu 90	Trp	Leu	Pro	Ile	Pro 95	His
5	Thr	Ala	Ile	Ile 100	Pro	Arg	Lys	Lys	Asp 105	Gln	Leu	Gly	Glu	Ala 110	Leu	Ser
	Gly	Phe	Val 115	Gly	Asp	Asn	Phe	Leu 120	Asn	Ala	Gln	Leu	Ile 125	Thr	Glu	Lys
10	Val	Ser 130	Gln	Ala	Arg	Ile	Pro 135	Glu	Arg	Ala	Gly	Glu 140	Trp	Leu	Ala	Gln
15	Pro 145	Glu	Asn	Gly	Glu	Lys 150	Val	Ser	Arg	Glu	Val 155	Gly	Lys	Leu	Thr	Ala 160
	Asn	Ile	Val	Arg	Ala 165	Ile	Asp	Pro	Ser	Asp 170	Ala	Glu	Ala	Val	Ile 175	Lys
20	Ser	Ala	Val	Ile 180	Asp	Lys	Leu	Ala	Glu 185	Pro	Thr	Trp	Gly	Pro 190	Pro	Ala
	Gly	Arg	Leu 195	Leu	Glu	Gln	Leu	Leu 200	Ala	Glu	Ala	Lys	Pro 205	Asn	Gln	Leu
25	Ser	Arg 210	Asn	Ser	Arg	Ser	Gly 215	Cys	Thr	Lys	Arg	Arg 220	Trp	Ala	Pro	Glu
30	Pro 225	Leu	Ile	Asp	Arg	Leu 230	Leu	Asn	Glu	Arg	Arg 235	Pro	Ile	Trp	Ala	Pro 240
30	Lys	Phe	Thr	Ala	Gln 245	Leu	Val	Ser	Gly	Lys 250	Val	Tyr	Asp	Glu	Val 255	Ile
35	Lys	Phe	Thr	Glu 260	Ala	Val	Ala	Ala	Asp 265	Pro	Asn	His	Glu	Ala 270	Arg	Lys
	Ser	Leu	Arg 275	Arg	Phe	Leu	Asn	Lys 280	Leu	Ala	Gln	Asp	Leu 285	Gln	His	Asp
40	Pro	Gly 290	Met	Ile	Ile	Lys	Val 295	Glu	Glu	Ile	Lys	Arg 300	Asp	Ile	Met	Gly
45	Ser 305	Gly	Ala	Ile	Ala	Gln 310	Ala	Ala	Pro	Thr	Ile 315	Trp	Ala	Ser	Ala	Ser 320
13	Glu	Ser	Leu	Ile	Glu 325	Ser	Ala	Glu	Asp	Glu 330	Ser	Ser	Ile	Leu	Arg 335	Arg
50	Lys	Ile	Ala	Glu 340	Ala	Ala	Thr	Ser	Trp 345	Gly	Gln	Arg	Leu	Leu 350	Val	Asp
	Asp	Ser	Leu 355	Arg	His	Ser	Leu	Asp 360	Thr	Arg	Ile	Thr	Gly 365	Ala	Ala	Ala
55	Phe	Leu 370	Ala	Asp	Asn	Tyr	Ala 375	Pro	Glu	Val	Thr	Gly 380	Ile	Ile	Ser	Glu
	Thr 385	Ile	Glu	Arg	Trp	Asp 390	Ala	Glu	Glu	Ala	Ser 395	Glu	Lys	Ile	Glu	Leu 400

	Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val 405 410 415												
5	Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe 420 425 430												
	Gly Ala												
10													
15	<210> 3 <211> 28 <212> DNA <213> Artificial sequence												
20	<220> <223> Description of the artificial sequence: Primer dep67-ex1												
	<400> 3 gaggtacctc caccctgcg tacataat	28											
25	<210> 4 <211> 28 <212> DNA <213> Artificial sequence												
30	<220> <223> Description of the artificial sequence: Primer dep67-ex2												
35	<400> 4 tgtctagact agttaagctc cgaagagg	28											